



10070412 . 031502

1

## SEQUENCE LISTING

&lt;110&gt; AstaCarotene AB

&lt;120&gt; DNA construct and its use

&lt;130&gt; 29295-AstaCarotene

<140>  
<141>

&lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

<210> 1  
<211> 2543  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: napin promoter  
+ chloroplast localization signal + beta-carotene C-4 oxygenase  
coding sequence + termination sequence

&lt;220&gt;

<221> promoter  
<222> (1)..(1145)

&lt;220&gt;

<221> transit\_peptide  
<222> (1179)..(1347)

&lt;220&gt;

<221> CDS  
<222> (1179)..(2217)

&lt;220&gt;

<221> terminator  
<222> (2273)..(2536)

&lt;400&gt; 1

aagtttctt catcggtat tgattccttt aaagacttat gtttcttata ttgcttctga 60  
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tttccaaacat tttaaatttc actattggct gaatgcttct tctttgagga agaaacaatt 180  
cagatggcag aaatgtatca accaatgcat atatacaaatt gtaccttgc ttctcaaaac 240  
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tcctctttat tactattttc atgcgagggtt gccatgtaca ttatatttgt aaggattgac 360  
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aactcaaatt cgattgacat gtatccattc aacataaaat taaaccagcc tgcacctgca 600  
tccacatttc aagtattttc aaaccgttcg gtccttatcc accgggtgta acaagacgga 660

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 tatgaagtta agtttttacc ttgttttaa aaagaatcgt tcataagatg ccatgccaga 900  
 acattagcta cacgttacac atagcatgca gccgcggaga attgttttc ttgcactt 960  
 gtcactccct tcaaacacct aagagcttct ctctcacagc acacacatac aatcacatgc 1020  
 gtgcacatgt tattacacgt gatgcacatg caaatctcct ttatagccta taaattaact 1080  
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 1 5  
 ctc tct tcc gct act atg gtt gcc tct ccg gct cag gcc act atg gtc 1242  
 Leu Ser Ser Ala Thr Met Val Ala Ser Pro Ala Gln Ala Thr Met Val  
 10 15 20  
 gct cct ttc aac gga ctt aag tcc tcc gct gcc ttc cca gcc acc cgc 1290  
 Ala Pro Phe Asn Gly Leu Lys Ser Ser Ala Ala Phe Pro Ala Thr Arg  
 25 30 35  
 aag gct aac aac gac att act tcc atc aca agc aac ggc gga cgc gtt 1338  
 Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser Asn Gly Gly Arg Val  
 40 45 50  
 aac tgc atg tct aga atg cca tcc gag tcg tca gac gca gct cgt cct 1386  
 Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro  
 55 60 65  
 gcg cta aag cac gcc tac aaa cct cca gca tct gac gca gct cgt cct 1434  
 Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile  
 70 75 80 85  
 acg atg gcg ctg acc atc att ggc acc tgg acc gca gtg ttt tta cac 1482  
 Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His  
 90 95 100  
 gca ata ttt caa atc agg cta ccg aca tcc atg gac cag ctt cac tgg 1530  
 Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp  
 105 110 115  
 ttg cct gtg tcc gaa gcc aca gcc cag ctt ttg ggc gga agc agc agc 1578  
 Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser  
 120 125 130  
 cta ctg cac atc gct gca gtc ttc att gta ctt gag ttc ctg tac act 1626  
 Leu Leu His Ile Ala Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr  
 135 140 145

ggt cta ttc atc acc aca cat gac gca atg cat ggc acc ata gct ttg	1674
Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Leu	
150 155 160 165	
agg cac agg cag ctc aat gat ctc ctt ggc aac atc tgc ata tca ctg	1722
Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu	
170 175 180	
tac gcc tgg ttt gac tac agc atg ctg cat cgc aag cac tgg gag cac	1770
Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg Lys His Trp Glu His	
185 190 195	
cac aac cat act ggc gaa gtg ggg aaa gac cct gac ttc cac aag gga	1818
His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly	
200 205 210	
aat ccc ggc ctt gtc ccc tgg ttc gcc agc ttc atg tcc agc tac atg	1866
Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
215 220 225	
tcc ctg tgg cag ttt gcc cggtt gca tgg tgg gca gtg gtg atg caa	1914
Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln	
230 235 240 245	
atg ctg ggg gcg ccc atg gca aat ctc cta gtc ttc atg gct gca gcc	1962
Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala	
250 255 260	
cca atc ttg tca gca ttc cgc ctc ttc tac ttc ggc act tac ctg cca	2010
Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro	
265 270 275	
cac aag cct gag cca ggc cct gca gca ggc tct cag gtg atg gcc tgg	2058
His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp	
280 285 290	
ttc agg gcc aag aca agt gag gca tct gat gtg atg agt ttc ctg aca	2106
Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr	
295 300 305	
tgc tac cac ttt gac ctg cac tgg gag cac cac aga tgg ccc ttt gcc	2154
Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala	
310 315 320 325	
ccc tgg tgg cag ctg ccc cac tgc cgc cgc ctg tcc ggg cgt ggc ctg	2202
Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu	
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Val Pro Ala Leu Ala	
345	
agtgtcatgg agctcgaatt tccccatcg ttcaaacatt tggcaataaa gtttcttaag	2317
attgaatcct gttgccggtc ttgcgatgtatcatataa tttctgttga attacgttaa	2377
gcatgtataa attaacatgt aatgcatgac gttatattatg agatgggttt ttatgattag	2437
agtcccgcaa ttatacattt aatacgcgat agaaaacaaa atatagcgcg caaactagga	2497
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<210> 2  
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<212> PRT  
 <213> Artificial Sequence  
 <223> Description of Artificial Sequence: deduced fusion protein of  
 transit peptide + peptide with beta-carotene C-4 oxygenase activity

<400> 2

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 20 25 30  
 Phe Pro Ala Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser  
 35 40 45  
 Asn Gly Gly Arg Val Asn Cys Met Ser Arg Met Pro Ser Glu Ser Ser  
 50 55 60  
 Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro Pro Ala Ser  
 65 70 75 80  
 Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly Thr Trp Thr  
 85 90 95  
 Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro Thr Ser Met  
 100 105 110  
 Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala Gln Leu Leu  
 115 120 125  
 Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe Ile Val Leu  
 130 135 140  
 Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His  
 145 150 155 160  
 Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu Leu Gly Asn  
 165 170 175  
 Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met Leu His Arg  
 180 185 190  
 Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro  
 195 200 205  
 Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala Ser Phe  
 210 215 220  
 Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala Trp Trp  
 225 230 235 240  
 Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn Leu Leu Val  
 245 250 255

Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe  
260 265 270

Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala Gly Ser  
275 280 285

Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser Asp Val  
290 295 300

Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His  
305 310 315 320

Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys Arg Arg Leu  
325 330 335

Ser Gly Arg Gly Leu Val Pro Ala Leu Ala  
340 345